

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Denney Jr., Dan W.
- (ii) TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And Leukemia
- (iii) NUMBER OF SEQUENCES: 77
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Medlen & Carroll, LLP
 - (B) STREET: 220 Montgomery Street, Suite 2200
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: United States Of America
 - (F) ZIP: 94104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/644,664
 - (B) FILING DATE: 01-MAY-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ingolia, Diane E.
 - (B) REGISTRATION NUMBER: 40,027
 - (C) REFERENCE/DOCKET NUMBER: DENNEY-02406
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 705-8410
 - (B) TELEFAX: (415) 397-8338

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTAGAGCGG CCGCGGAGGC CGAATTCG

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCCGAATT CGGCCTCCGC GGCCGCTCTA GATGCA

36

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 677 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGATCCAGAC ATGATAAGAT ACATTGATGA GTTTGGACAA ACCACAAC TA GAATGCAGTG 60
AAAAAATGC TTTATTTGTG AAATTTGTGA TGCTATTGCT TTATTTGTAA CCATTATAAG 120
CTGCAATAAA CAAGTTAACA ACAACAATTG CATTCAATTT ATGTTTCAGG TTCAGGGGGA 180
GGTGTGGGAG GTTTTTTAAA GCAAGTAAAA CCTCTACAAA TGTGGTATGG CTGATTATGA 240
TCATGAACAG ACTGTGAGGA CTGAGGGGCC TGAAATGAGC CTTGGGACTG TGAATCAATG 300
CCTGTTTCAT GCCCTGAGTC TTCCATGTTT TTCTCCCCAC CATCTTCATT TTTATCAGCA 360
TTTTCTGGC TGTCTTCATC ATCATCATCA CTGTTTCTTA GCCAATCTAA AACTCCAATT 420
CCCATAGCCA CATTAACTT CATTTTTTGA TACACTGACA AACTAACTC TTTGTCCAAT 480
CTCTCTTTCC ACTCCACAAT TCTGCTCTGA ATACTTTGAG CAACTCAGC CACAGGTCTG 540
TACCAAATTA ACATAAGAAG CAAAGCAATG CCACTTTGAA TTATTCTCTT TTCTAACAAA 600
AACTCACTGC GTTCCAGGCA ATGCTTTAAA TAATCTTTGG GCCTAAAATC TATTTGTTTT 660
ACAAATCTGG CCTGCAG 677

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTAGAATTCA CGCGTAGGCC TCCGCGGCCG CGCGCATGC

39

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AATTGCATGC GCGCGGCCGC GGAGGCCTAC GCGTGAATT

39

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 633 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAAGCTTGCT GTGGAATGTG TGTCAGTTAG GGTGTGGAAA GTCCCCAGGC TCCCCAGCAG 60

GCAGAAGTAT GCAAAGCATG CATCTCAATT AGTCAGCAAC CAGGTGTGGA AAGTCCCCAG 120

GCTCCCCAGC AGGCAGAAGT ATGCAAAGCA TGCATCTCAA TTAGTCAGCA ACCATAGTCC 180

CGCCCCTAAC TCCGCCCATC CCGCCCCCTAA CTCCGCCCAG TTCCGCCCAT TCTCCGCCCC 240

ATGGCTGACT AATTTTTTTTT ATTTATGCAG AGGCCGAGGC CGCCTCGGCC TCTGAGCTAT 300

TCCAGAAGTA GTGAGGAGGC TTTTGTGGAG GCCTAGGCTT TTGCAAAAAG CTCCTCGAGC 360

TCGCATCTCT CCTTCACGCG CCCGCCGCC TACCTGAGGC CGCCATCCAC GCCGGTTGAG 420

TCGCGTTCTG CCGCCTCCCG CCTGTGGTGC CTCCTGAACT GCGTCCGCCG TCTAGGTAAG 480

TTTAGAGCTC AGGTCGAGAC CGGGCCTTTG TCCGCGCTC CCTTGGAGCC TACCTAGACT 540

CAGCCGGCTC TCCACGCTTT GCCTGACCCT GCTTGCTCAA CTCTACGTCT TTGTTTCGTT 600

TTCTGTTCTG CGCCGTTACA GATCGCCTCG AGG 633

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 635 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAAGCTTGCG ATTAGTCCAA TTTGTTAAAG ACAGGATATC AGTGGTCCAG GCTCTAGTTT	60
TGACTCAACA ATATCACCAG CTGAAGCCTA TAGAGTACGA GCCATAGATA AAATAAAAGA	120
TTTTATTTAG TCTCCAGAAA AAGGGGGGAA TGAAAGACCC CACCTGTAGG TTTGGCAAGC	180
TAGCTTAAGT AACGCCATTT TGCAAGGCAT GGAAAAATAC ATAAGTGAAGA ATAGAGAAAGT	240
TCAGATCAAG GTCAGGAACA GATGGAACAG CTGAATATGG GCCAAACAGG ATATCTGTGG	300
TAAGCAGTTC CTGCCCCGGC TCAGGGCCAA GAACAGATGG AACAGCTGAA TATGGGCCAA	360
ACAGGATATC TGTGGTAAGC AGTTCCTGCC CCGGCTCAGG GCCAAGAACA GATGGTCCCC	420
AGATGCGGTC CAGCCCTCAG CAGTTTCTAG AGAACCATCA GATGTTTCCA GGGTGCCCCA	480
AGGACCTGAA ATGACCCTGT GCCTTATTTG AACTAACCAA TCAGTTCGCT TCTCGCTTCT	540
GTTCGCGCGC TTCTGCTCCC CGAGCTCAAT AAAAGAGCCC ACAACCCCTC ACTCGGGGCG	600
CCAGTCCTCC GATTGACTGA GTCGCCCCCT CGAGG	635

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGCTTTGGA GCTAAGCCAG CAATGGTAGA GGAAGATTC TGCACGTCCC TTCCAGGCGG	60
CCTCCCCGTC ACCACCCCCC CCAACCCGCC CCGACCGGAG CTGAGAGTAA TTCATACAAA	120
AGGACTCGCC CCTGCCTTGG GGAATCCAG GGACCGTCGT TAAACTCCCA CTAACGTAGA	180
ACCCAGAGAT CGCTGCGTTC CCGCCCCCTC ACCCGCCCGC TCTCGTCATC ACTGAGGTGG	240
AGAAGAGCAT GCGTGAGGCT CCGGTGCCCCG TCAGTGGGCA GAGCGCACAT CGCCCACAGT	300
CCCCGAGAAG TTGGGGGGAG GGGTCGGCAA TTGAACCGGT GCCTAGAGAA GGTGGCGCGG	360
GGTAAACTGG GAAAGTGATG TCGTGACTG GCTCCGCCCTT TTTCCCGAGG GTGGGGGAGA	420
ACCGTATATA AGTGCAGTAG TCGCCGTGAA CGTTCCTTTT CGCAACGGGT TTGCCGCCCTC	480
GAG	483

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGCTTTGGA GCTAAGCCAG CAAT

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(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTCGAGGCGG CAAACCCGTT GCG

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(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAGCTTTGGA GCTAAGCCAG CAATGGTAGA GGAAGATTC TGCACGTCCC TTCCAGGCGG 60
CCTCCCCGTC ACCACCCCC CCAACCCGCC CCGACCGGAG CTGAGAGTAA TTCATACAAA 120
AGGACTCGCC CCTGCCTTGG GGAATCCCAG GGACCGTCGT TAAACTCCCA CTAACGTAGA 180
ACCCAGAGAT CGCTGCGTTC CCGCCCCCTC ACCCGCCCGC TCTCGTCATC ACTGAGGTGG 240
AGAAGAGCCA TGC GTGAGGC TCCGGTGCCC GTCAGTGGGC AGAGCGCACA TCGCCCACAG 300
TCCCCGAGAA GTTGGGGGGA GGGGTCGGCA ATTGAACCGG TGCC TAGAGA AGGTGGCGCG 360
GGGTAACTG GGAAAGTGAT GTCGTGTACT GGCTCCGCCT TTTTCCCGAG GGTGGGGGAG 420
AACCCGTATA TAAGTGCAGT AGTCGCCGTG AACGTTCTTT TTCGCAACGG GTTTGCCGCC 480
AGAACACAGG TAAGTGCCGT GTGTGGTTCC CGCGGGCCTG GCCTCTTTAC GGGTTATGGC 540
CCTTGCGTGC CTTGAATTAC TTCCACGCCC CTGGCTGCAG TACGTGATTC TTGATCCCGA 600
GCTTCGGGTT GGAAGTGGGT GGGAGAGTTC GAGGCCTTGC GCTTAAGGAG CCCCTTCGCC 660

TCGTGCTTGA GTTGAGGCCT GGCCTGGGCG CTGGGGCCCC CGCGTGC GAA TCTGGTGGCA	720
CCTTCGCGCC TGTCTCGCTG CTTTCGATAA GTCTCTAGCC ATTTAAAATT TTTGATGACC	780
TGCTGCGACG CTTTTTTTCT GGCAAGATAG TCTTGTAAT GCGGGCCAAG ATCTGCACAC	840
TGGTATTTTCG GTTTTTGGGG CCGCGGGCGG CGACGGGGCC CGTGCGTCCC AGCGCACATG	900
TTGGCGGAGG CGGGGCCTGC GAGCGCGGCC ACCGAGAATC GGACGGGGGT AGTCTCAAGC	960
TGGCCGGCCT GCTCTGGTGC CTGGCCTCGC GCCGCCGTGT ATCGCCCCGC CCTGGGCGGC	1020
AAGGCTGGCC CGGTCGGCAC CAGTTGCGTG AGCGGAAAGA TGGCCGCTTC CCGGCCCTGC	1080
TGCAGGGAGC TCAAATGGA GGACGCGGCG CTCGGGAGAG CGGGCGGGTG AGTCACCCAC	1140
ACAAAGGAAA AGGGCCTTTC CGTCCTCAGC CGTCGCTTCA TGTGACTCCA CGGAGTACCG	1200
GGCGCCGTCC AGGCACCTCG ATTAGTTCTC GAGCTTTTGG AGTACGTCGT CTTTAGGTTG	1260
GGGGGAGGGG TTTTATGCGA TGGAGTTTCC CCACACTGAG TGGGTGGAGA CTGAAGTTAG	1320
GCCAGCTTGG CACTTGATGT AATTCTCCTT GGAATTTGCC CTTTTTGAGT TTGGATCTTG	1380
GTTCAATTCTC AAGCCTCAGA CAGTGGTTCA AAGTTTTTTT CTTCCATTTC AGGTGTCGTG	1440
AAAACCTCTAG A	1451

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCTAGAGTTT TCACGACACC TGA

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(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 88..741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTACCTCACT GCTTTCCGGA GCGGTAGCAC CTCCTCCGCC GGCTTCCTCC TCAGACCGCT

60

TTTTGCCGCG AGCCGACCGG TCCCGTC ATG CCG ACC CGC AGT CCC AGC GTC	111
Met Pro Thr Arg Ser Pro Ser Val	
1 5	
GTG ATT AGC GAT GAT GAA CCA GGT TAT GAC CTA GAT TTG TTT TGT ATA	159
Val Ile Ser Asp Asp Glu Pro Gly Tyr Asp Leu Asp Leu Phe Cys Ile	
10 15 20	
CCT AAT CAT TAT GCC GAG GAT TTG GAA AAA GTG TTT ATT CCT CAT GGA	207
Pro Asn His Tyr Ala Glu Asp Leu Glu Lys Val Phe Ile Pro His Gly	
25 30 35 40	
CTG ATT ATG GAC AGG ACT GAA AGA CTT GCT CGA GAT GTC ATG AAG GAG	255
Leu Ile Met Asp Arg Thr Glu Arg Leu Ala Arg Asp Val Met Lys Glu	
45 50 55	
ATG GGA GGC CAT CAC ATT GTG GCC CTC TGT GTG CTC AAG GGG GGC TAT	303
Met Gly Gly His His Ile Val Ala Leu Cys Val Leu Lys Gly Gly Tyr	
60 65 70	
AAG TTC TTT GCT GAC CTG CTG GAT TAC ATT AAA GCA CTG AAT AGA AAT	351
Lys Phe Phe Ala Asp Leu Leu Asp Tyr Ile Lys Ala Leu Asn Arg Asn	
75 80 85	
AGT GAT AGA TCC ATT CCT ATG ACT GTA GAT TTT ATC AGA CTG AAG AGC	399
Ser Asp Arg Ser Ile Pro Met Thr Val Asp Phe Ile Arg Leu Lys Ser	
90 95 100	
TAC TGT AAT GAT CAG TCA ACG GGG GAC ATA AAA GTT ATT GGT GGA GAT	447
Tyr Cys Asn Asp Gln Ser Thr Gly Asp Ile Lys Val Ile Gly Gly Asp	
105 110 115 120	
GAT CTC TCA ACT TTA ACT GGA AAG AAT GTC TTG ATT GTT GAA GAT ATA	495
Asp Leu Ser Thr Leu Thr Gly Lys Asn Val Leu Ile Val Glu Asp Ile	
125 130 135	
ATT GAC ACT GGT AAA ACA ATG CAA ACT TTG CTT TCC CTG GTT AAG CAG	543
Ile Asp Thr Gly Lys Thr Met Gln Thr Leu Leu Ser Leu Val Lys Gln	
140 145 150	
TAC AGC CCC AAA ATG GTT AAG GTT GCA AGC TTG CTG GTG AAA AGG ACC	591
Tyr Ser Pro Lys Met Val Lys Val Ala Ser Leu Leu Val Lys Arg Thr	
155 160 165	
TCT CGA AGT GTT GGA TAC AGG CCA GAC TTT GTT GGA TTT GAA ATT CCA	639
Ser Arg Ser Val Gly Tyr Arg Pro Asp Phe Val Gly Phe Glu Ile Pro	
170 175 180	
GAC AAG TTT GTT GTT GGA TAT GCC CTT GAC TAT AAT GAG TAC TTC AGG	687
Asp Lys Phe Val Val Gly Tyr Ala Leu Asp Tyr Asn Glu Tyr Phe Arg	
185 190 195 200	
AAT TTG AAT CAC GTT TGT GTC ATT AGT GAA ACT GGA AAA GCC AAA TAC	735
Asn Leu Asn His Val Cys Val Ile Ser Glu Thr Gly Lys Ala Lys Tyr	
205 210 215	
AAA GCC TAAGATGAGC GCAAGTTGAA TCTGCAAATA CGAGGAGTCC TGTTGATGTT	791
Lys Ala	
GCCAGTAAAA TTAGCAGGTG TTCTAGTCCT GTGGCCATCT GCCTAGTAAA GCTTTTTTGCA	851

TGAACCTTCT ATGAATGTTA CTGTTTTATT TTTAGAAATG TCAGTTGCTG CGTCCCCAGA 911
 CTTTTGATTT GCACTATGAG CCTATAGGCC AGCCTACCCCT CTGGTAGATT GTCGCTTATC 971
 TTGTAAGAAA AACAAATCTC TTAAATTACC ACTTTTAAAT AATAATACTG AGATTGTATC 1031
 TGTAAGAAGG ATTTAAAGAG AAGCTATATT AGTTTTTTAA TTGGTATTTT AATTTTTATA 1091
 TATTCAGGAG AGAAAGATGT GATTGATATT GTTAATTTAG ACGAGTCTGA AGCTCTCGAT 1151
 TTCCTATCAG TAACAGCATC TAAGAGGTTT TGCTCAGTGG AATAAACATG TTTCAGCAGT 1211
 GTTGGCTGTA TTTTCCCACT TTCAGTAAAT CGTTGTCAAC AGTTCCTTTT AAATGCAAAT 1271
 AAATAAATTC TAAAAATT 1289

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Pro Thr Arg Ser Pro Ser Val Val Ile Ser Asp Asp Glu Pro Gly
 1 5 10 15
 Tyr Asp Leu Asp Leu Phe Cys Ile Pro Asn His Tyr Ala Glu Asp Leu
 20 25 30
 Glu Lys Val Phe Ile Pro His Gly Leu Ile Met Asp Arg Thr Glu Arg
 35 40 45
 Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His Ile Val Ala
 50 55 60
 Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Phe Ala Asp Leu Leu Asp
 65 70 75 80
 Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr
 85 90 95
 Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly
 100 105 110
 Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys
 115 120 125
 Asn Val Leu Ile Val Glu Asp Ile Ile Asp Thr Gly Lys Thr Met Gln
 130 135 140
 Thr Leu Leu Ser Leu Val Lys Gln Tyr Ser Pro Lys Met Val Lys Val
 145 150 155 160
 Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Val Gly Tyr Arg Pro
 165 170 175
 Asp Phe Val Gly Phe Glu Ile Pro Asp Lys Phe Val Val Gly Tyr Ala
 180 185 190

Leu Asp Tyr Asn Glu Tyr Phe Arg Asn Leu Asn His Val Cys Val Ile
 195 200 205

Ser Glu Thr Gly Lys Ala Lys Tyr Lys Ala
 210 215

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCATGCGCGC GGCCGCGGAG GCTTTTTTTT TTTTTTTTTT

40

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGCAACGCG TGCCATCATG GTTCGAC

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGGCAGCGGC CGCATAGATC TAAAGCCAGC

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(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 671 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 13..573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACGCGTGCCA TC ATG GTT CGA CCA TTG AAC TGC ATC GTC GCC GTG TCC	48
Met Val Arg Pro Leu Asn Cys Ile Val Ala Val Ser	
1 5 10	
CAA AAT ATG GGG ATT GGC AAG AAC GGA GAC CTA CCC TGG CCT CCG CTC	96
Gln Asn Met Gly Ile Gly Lys Asn Gly Asp Leu Pro Trp Pro Pro Leu	
15 20 25	
AGG AAC GAG TTC AAG TAC TTC CAA AGA ATG ACC ACA ACC TCT TCA GTG	144
Arg Asn Glu Phe Lys Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val	
30 35 40	
GAA GGT AAA CAG AAT CTG GTG ATT ATG GGT AGG AAA ACC TGG TTC TCC	192
Glu Gly Lys Gln Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser	
45 50 55 60	
ATT CCT GAG AAG AAT CGA CCT TTA AAG GAC AGA ATT AAT ATA GTT CTC	240
Ile Pro Glu Lys Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu	
65 70 75	
AGT AGA GAA CTC AAA GAA CCA CCA CGA GGA GCT CAT TTT CTT GCC AAA	288
Ser Arg Glu Leu Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys	
80 85 90	
AGT TTG GAT GAT GCC TTA AGA CTT ATT GAA CAA CCG GAA TTG GCA AGT	336
Ser Leu Asp Asp Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser	
95 100 105	
AAA GTA GAC ATG GTT TGG ATA GTC GGA GGC AGT TCT GTT TAC CAG GAA	384
Lys Val Asp Met Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu	
110 115 120	
GCC ATG AAT CAA CCA GGC CAC CTT AGA CTC TTT GTG ACA AGG ATC ATG	432
Ala Met Asn Gln Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met	
125 130 135 140	
CAG GAA TTT GAA AGT GAC ACG TTT TTC CCA GAA ATT GAT TTG GGG AAA	480
Gln Glu Phe Glu Ser Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys	
145 150 155	
TAT AAA CTT CTC CCA GAA TAC CCA GGC GTC CTC TCT GAG GTC CAG GAG	528
Tyr Lys Leu Leu Pro Glu Tyr Pro Gly Val Leu Ser Glu Val Gln Glu	
160 165 170	
GAA AAA GGC ATC AAG TAT AAG TTT GAA GTC TAC GAG AAG AAA GAC	573
Glu Lys Gly Ile Lys Tyr Lys Phe Glu Val Tyr Glu Lys Lys Asp	
175 180 185	
TAACAGGAAG ATGCTTTCAA GTTCTCTGCT CCCCTCCTAA AGCTATGCAT TTTTATAAGA	633
CCATGGGACT TTTGCTGGCT TTAGATCTAT GCGGCCGC	671

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Val Arg Pro Leu Asn Cys Ile Val Ala Val Ser Gln Asn Met Gly
1 5 10 15
Ile Gly Lys Asn Gly Asp Leu Pro Trp Pro Pro Leu Arg Asn Glu Phe
20 25 30
Lys Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val Glu Gly Lys Gln
35 40 45
Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile Pro Glu Lys
50 55 60
Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser Arg Glu Leu
65 70 75 80
Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser Leu Asp Asp
85 90 95
Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys Val Asp Met
100 105 110
Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala Met Asn Gln
115 120 125
Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln Glu Phe Glu
130 135 140
Ser Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys Tyr Lys Leu Leu
145 150 155 160
Pro Glu Tyr Pro Gly Val Leu Ser Glu Val Gln Glu Glu Lys Gly Ile
165 170 175
Lys Tyr Lys Phe Glu Val Tyr Glu Lys Lys Asp
180 185

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATATATCTAG ACCACCATGC CTGGCTCAGC ACTG

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(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATTATTGCGG CCGCTTAGCT TTTCATTTTG ATCAT

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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTCTAGAGC CAAATAAAGG AAGTGGAACC ACTTCAGGTA CTACCCGTCT TCTATCTGGG 60
CACACGTGTT TCACGTTGAC AGGTTTGCTT GGGACGCTAG TAACCATGGG CTTGCTGACT 120
TAGGCATCGA ATTC 134

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAATTCGATG CCTAAGTCAG CAAGCCCATG GTTACTAGCG TCCCAAGCAA ACCTGTCAAC 60
GTGAAACACG TGTGCCCAGA TAGAAGACGG GTAGTACCTG AAGTGGTTCC ACTTCCTTTA 120
TTTGGCTCTA GACC 134

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TAATACGACT CACTATAGGG CGAATTGGAG CTCCACCGCG GTGGCGGCCG CTCTAGAACT 60
AGTGGATCCC CCGGGCTGCA GGAATTCGAT GGTCTAGAGC CAAATAAAGG AAGTGGAACC 120
ACTTCAGGTA CTACCCGTCT TCTATCTGGG CACACGTGTT TCACGTTGAC AGGTTTGCTT 180
GGGACGCTAG TAACCATGGG CTTGCTGACT TAGGCATCGA ATTCATCAAG CTTATCGATA 240
CCGTCGACCT CGAGGGGGGG CCCGGTACCC AGCTTTTGTT CCCTTTAGTG AGGGTTAATT 300

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCACTTCCTT TATTTGGGAG AGGGCTTG

28

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATG GCC ATA AGT GGA GTC CCT GTG CTA GGA TTT TTC ATC ATA GCT GTG	48
Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val	
1 5 10 15	
CTG ATG AGC GCT CAG GAA TCA TGG GCT ATC AAA GAA GAA CAT GTG ATC	96
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile	
20 25 30	
ATC CAG GCC GAG TTC TAT CTG AAT CCT GAC CAA TCA GGC GAG TTT ATG	144
Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met	
35 40 45	
TTT GAC TTT GAT GGT GAT GAG ATT TTC CAT GTG GAT ATG GCA AAG AAG	192
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys	
50 55 60	
GAG ACG GTC TGG CGG CTT GAA GAA TTT GGA CGA TTT GCC AGC TTT GAG	240
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu	
65 70 75 80	
GCT CAA GGT GCA TTG GCC AAC ATA GCT GTG GAC AAA GCC AAC TTG GAA	288
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu	
85 90 95	
ATC ATG ACA AAG CGC TCC AAC TAT ACT CCG ATC ACC AAT GTA CCT CCA	336
Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro	
100 105 110	
GAG GTA ACT GTG CTC ACG AAC AGC CCT GTG GAA CTG AGA GAG CCC AAC	384
Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn	
115 120 125	

GTC	CTC	ATC	TGT	TTC	ATA	GAC	AAG	TTC	ACC	CCA	CCA	GTG	GTC	AAT	GTC	432
Val	Leu	Ile	Cys	Phe	Ile	Asp	Lys	Phe	Thr	Pro	Pro	Val	Val	Asn	Val	
130						135					140					
ACG	TGG	CTT	CGA	AAT	GGA	AAA	CCT	GTC	ACC	ACA	GGA	GTG	TCA	GAG	ACA	480
Thr	Trp	Leu	Arg	Asn	Gly	Lys	Pro	Val	Thr	Thr	Gly	Val	Ser	Glu	Thr	
145					150					155					160	
GTC	TTC	CTG	CCC	AGG	GAA	GAC	CAC	CTT	TTC	CGC	AAG	TTC	CAC	TAT	CTC	528
Val	Phe	Leu	Pro	Arg	Glu	Asp	His	Leu	Phe	Arg	Lys	Phe	His	Tyr	Leu	
				165				170						175		
CCC	TTC	CTG	CCC	TCA	ACT	GAG	GAC	GTT	TAC	GAC	TGC	AGG	GTG	GAG	CAC	576
Pro	Phe	Leu	Pro	Ser	Thr	Glu	Asp	Val	Tyr	Asp	Cys	Arg	Val	Glu	His	
			180					185					190			
TGG	GGC	TTG	GAT	GAG	CCT	CTT	CTC	AAG	CAC	TGG	GAG	TTT	GAT	GCT	CCA	624
Trp	Gly	Leu	Asp	Glu	Pro	Leu	Leu	Lys	His	Trp	Glu	Phe	Asp	Ala	Pro	
	195					200						205				
AGC	CCT	CTC	CCA	AAT	AAA	GGA	AGT	GGA	ACC	ACT	TCA	GGT	ACT	ACC	CGT	672
Ser	Pro	Leu	Pro	Asn	Lys	Gly	Ser	Gly	Thr	Thr	Ser	Gly	Thr	Thr	Arg	
	210					215					220					
CTT	CTA	TCT	GGG	CAC	ACG	TGT	TTC	ACG	TTG	ACA	GGT	TTG	CTT	GGG	ACG	720
Leu	Leu	Ser	Gly	His	Thr	Cys	Phe	Thr	Leu	Thr	Gly	Leu	Leu	Gly	Thr	
225					230				235					240		
CTA	GTA	ACC	ATG	GGC	TTG	CTG	ACT	TAG								747
Leu	Val	Thr	Met	Gly	Leu	Leu	Thr									
				245												

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Ala	Ile	Ser	Gly	Val	Pro	Val	Leu	Gly	Phe	Phe	Ile	Ile	Ala	Val
1				5					10					15	
Leu	Met	Ser	Ala	Gln	Glu	Ser	Trp	Ala	Ile	Lys	Glu	Glu	His	Val	Ile
			20					25					30		
Ile	Gln	Ala	Glu	Phe	Tyr	Leu	Asn	Pro	Asp	Gln	Ser	Gly	Glu	Phe	Met
		35					40					45			
Phe	Asp	Phe	Asp	Gly	Asp	Glu	Ile	Phe	His	Val	Asp	Met	Ala	Lys	Lys
	50					55					60				
Glu	Thr	Val	Trp	Arg	Leu	Glu	Glu	Phe	Gly	Arg	Phe	Ala	Ser	Phe	Glu
65					70				75					80	
Ala	Gln	Gly	Ala	Leu	Ala	Asn	Ile	Ala	Val	Asp	Lys	Ala	Asn	Leu	Glu
			85					90						95	

Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
100 105 110

Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
115 120 125

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
130 135 140

Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
145 150 155 160

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
165 170 175

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
180 185 190

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
195 200 205

Ser Pro Leu Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg
210 215 220

Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr
225 230 235 240

Leu Val Thr Met Gly Leu Leu Thr
245

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCACTTCCTT TATTTGGTGC AGATTCAG

28

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 786 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATG GTG TGT CTG AAG CTC CCT GGA GGC TCC TGC ATG ACA GCG CTG ACA	48
Met Val Cys Leu Lys Leu Pro Gly Gly Ser Cys Met Thr Ala Leu Thr	
1 5 10 15	
GTG ACA CTG ATG GTG CTG AGC TCC CGA CTG GCT TTG GCT GGG GAC ACC	96
Val Thr Leu Met Val Leu Ser Ser Arg Leu Ala Leu Ala Gly Asp Thr	
20 25 30	
CGA CCA CGT TTC TTG TGG CAG CTT AAG TTT GAA TGT CAT TTC TTC AAT	144
Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu Cys His Phe Phe Asn	
35 40 45	
GGG ACG GAG CGG GTG CGG TTG CTG GAA AGA TGC ATC TAT AAC CAA GAG	192
Gly Thr Glu Arg Val Arg Leu Leu Glu Arg Cys Ile Tyr Asn Gln Glu	
50 55 60	
GAG TCC GTG CGC TTC GAC AGC GAC GTG GGG GAG TAC CGG GCG GTT GAG	240
Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Glu	
65 70 75 80	
GAG CTG GGG CGG CCT GAT GCC GAG TAC TGG AAC AGC CAG AAG GAC CTC	288
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu	
85 90 95	
CTG GAG CAG AAG CGG GGC CAG GTG GAC AAT TAC TGC AGA CAC AAC TAC	336
Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr	
100 105 110	
GGG GTT GGT GAG AGC TTC ACA GTG CAG CGG CGA GTT GAG CCT AAG GTG	384
Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val	
115 120 125	
ACT GTG TAT CCT TCA AAG ACC CAG CCC CTG CAG CAC CAC AAC CTC CTG	432
Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu	
130 135 140	
GTC TGC TCT GTG AGT GGT TTC TAT CCA GGC AGC ATT GAA GTC AGG TGG	480
Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp	
145 150 155 160	
TTC CGG AAC GGC CAG GAA GAG AAG GCT GGG GTG GTG TCC ACG GGC CTG	528
Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu	
165 170 175	
ATC CAG AAT GGA GAT TGG ACC TTC CAG ACC CTG GTG ATG CTG GAA ATA	576
Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Ile	
180 185 190	
GTT CCT CGG AGT GGA GAG GTT TAC ACC TGC CAA GTG GAG CAC CCA AGT	624
Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser	
195 200 205	
GTG ACG AGC CCT CTC ACA GTG GAA TGG AGA GCA CGG TCT GAA TCT GCA	672
Val Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala	
210 215 220	
CCA AAT AAA GGA AGT GGA ACC ACT TCA GGT ACT ACC CGT CTT CTA TCT	720
Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser	
225 230 235 240	

GGG CAC ACG TGT TTC ACG TTG ACA GGT TTG CTT GGG ACG CTA GTA ACC 768
 Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
 245 250 255

ATG GGC TTG CTG ACT TAG 786
 Met Gly Leu Leu Thr
 260

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Val	Cys	Leu	Lys	Leu	Pro	Gly	Gly	Ser	Cys	Met	Thr	Ala	Leu	Thr	1	5	10	15
Val	Thr	Leu	Met	Val	Leu	Ser	Ser	Arg	Leu	Ala	Leu	Ala	Gly	Asp	Thr	20	25	30	
Arg	Pro	Arg	Phe	Leu	Trp	Gln	Leu	Lys	Phe	Glu	Cys	His	Phe	Phe	Asn	35	40	45	
Gly	Thr	Glu	Arg	Val	Arg	Leu	Leu	Glu	Arg	Cys	Ile	Tyr	Asn	Gln	Glu	50	55	60	
Glu	Ser	Val	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Glu	65	70	75	80
Glu	Leu	Gly	Arg	Pro	Asp	Ala	Glu	Tyr	Trp	Asn	Ser	Gln	Lys	Asp	Leu	85	90	95	
Leu	Glu	Gln	Lys	Arg	Gly	Gln	Val	Asp	Asn	Tyr	Cys	Arg	His	Asn	Tyr	100	105	110	
Gly	Val	Gly	Glu	Ser	Phe	Thr	Val	Gln	Arg	Arg	Val	Glu	Pro	Lys	Val	115	120	125	
Thr	Val	Tyr	Pro	Ser	Lys	Thr	Gln	Pro	Leu	Gln	His	His	Asn	Leu	Leu	130	135	140	
Val	Cys	Ser	Val	Ser	Gly	Phe	Tyr	Pro	Gly	Ser	Ile	Glu	Val	Arg	Trp	145	150	155	160
Phe	Arg	Asn	Gly	Gln	Glu	Glu	Lys	Ala	Gly	Val	Val	Ser	Thr	Gly	Leu	165	170	175	
Ile	Gln	Asn	Gly	Asp	Trp	Thr	Phe	Gln	Thr	Leu	Val	Met	Leu	Glu	Ile	180	185	190	
Val	Pro	Arg	Ser	Gly	Glu	Val	Tyr	Thr	Cys	Gln	Val	Glu	His	Pro	Ser	195	200	205	
Val	Thr	Ser	Pro	Leu	Thr	Val	Glu	Trp	Arg	Ala	Arg	Ser	Glu	Ser	Ala	210	215	220	

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
225 230 235 240

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
245 250 255

Met Gly Leu Leu Thr
260

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTG GAT CCA CGA TCG TTT CTA TTG CGC AAT CCA AAT GAT AAG TAC GAA	48
Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu	
1 5 10 15	
CCA TTT TGG GAA GAT ACT ACA GAG AAC GTG GTG TGT GCC CTG GGC CTG	96
Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu	
20 25 30	
ACT GTG GGT CTG GTG GGC ATC ATT ATT GGG ACC ATC TTC ATC ATC AAG	144
Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys	
35 40 45	
GGA GTG CGC AAA AGC AAT GCA GCA GAA CGC AGG GGG CCT CTG	186
Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu	
50 55 60	
TAA	189

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu	
1 5 10 15	
Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu	
20 25 30	

Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys
 35 40 45

Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu
 50 55 60

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTG GAT CCA CGA TCG TTT CTA TTG CGC AAT CCA AAT GAT AAG TAC GAA	48
Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu	
1 5 10 15	
CCA TTT TGG GAA GAT CAG AGC AAG ATG CTG AGT GGA GTC GGG GGC TTC	96
Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe	
20 25 30	
GTG CTG GGC CTG CTC TTC CTT GGG GCC GGG CTG TTC ATC TAC TTC AGG	144
Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg	
35 40 45	
AAT CAG AAA GGA CAC TCT GGA CTT CAG CCA ACA GGA TTC CTG AGC	189
Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser	
50 55 60	
TGA	192

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu	
1 5 10 15	
Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe	
20 25 30	
Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg	
35 40 45	
Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser	
50 55 60	

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CGATCGTGGA TCCAAGTTTA GGTTCGTATC TGTTTCAAA

39

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGATCGAGGA TCCAAGATGG TGGCAGACAG GACC

34

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ACGCGTCCAC CATGGCCATA AGTGGAGTCC CT

32

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGATCCAAC CTGTAGTCTC TGGGAGAG

28

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ACGCGTCCAC CATGGTGTGT CTGAAGCTCC TG

32

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGATCCAAC TGCTCTGTGC AGATTCAGA

29

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAATTCTTTT TTGCGTGTGG CAGTTTAAAG TTATTAGTTT TAAAATCAG TACTTTTTAA

60

TGGAAACAAC TTGACCAAAA ATTTGTCACA GAATTTTGAG ACCCATTAAG AAAGTTAAAT

120

GAGAAACCTG TGTGTTCTT TGGTCAACAC CGAGACATT AGGTGAAAGA CATCTAATTC

180

TGGTTTTACG AATCTGAAA CTTCTTGAAA ATGTAATTCT TGAGTTAACA CTTCTGGGTG

240

GAGAATAGGG TTGTTTTCCC CCCACATAAT TGGAAGGGGA AGGAATATCG AT

292

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCGATGGCGC GCCTTAATTA

20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AGCTTAATTA AGGCGCGCCA

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..1137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCGGCC GCG TCG ACC AAG GGC CCC AGC GTG TTC CCC CTG GCC CCC TGC	48
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys	
1 5 10	
TCC CGC AGC ACC AGC GGC GGC ACC GCC GCC CTG GGC TGC CTG GTG AAG	96
Ser Arg Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys	
15 20 25 30	
GAC TAC TTC CCC GAG CCC GTG ACC GTG AGC TGG AAC AGC GGC GCC CTG	144
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu	
35 40 45	
ACC AGC GGC GTC CAC ACC TTC CCC GCC GTG CTG CAG TCC AGC GGC CTG	192
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu	
50 55 60	
TAC TCC CTG AGC AGC GTG GTG ACC GTG CCC AGC AGC AGC CTG GGC ACC	240
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
65 70 75	
CAG ACC TAC ACC TGC AAC GTG AAC CAC AAG CCC AGC AAC ACC AAG GTG	288
Gln Thr Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val	
80 85 90	
GAC AAG CGC GTG GAG CTG AAG ACC CCC CTG GGC GAC ACC ACC CAC ACC	336
Asp Lys Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr	
95 100 105 110	

TGC CCC CGC TGC CCC GAG CCC AAG AGC TGC GAC ACC CCT CCC CCC TGC	384
Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Cys	
115 120 125	
CCC CGC TGC CCC GAG CCC AAG AGC TGC GAC ACC CCT CCC CCC TGC CCC	432
Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro	
130 135 140	
CGC TGC CCC GAG CCC AAG AGC TGC GAC ACC CCT CCC CCC TGC CCC CGC	480
Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg	
145 150 155	
TGC CCC GCC CCC GAG CTG CTG GGC GGC CCC AGC GTG TTC CTG TTC CCC	528
Cys Pro Ala Pro Glu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro	
160 165 170	
CCC AAG CCC AAG GAC ACC CTG ATG ATC TCC CGC ACC CCC GAG GTG ACC	576
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr	
175 180 185 190	
TGC GTG GTG GTG GAC GTG AGC CAC GAG GAC CCC GAG GTG CAG TTC AAG	624
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys	
195 200 205	
TGG TAC GTG GAC GGC GTG GAG GTG CAT AAC GCC AAG ACC AAG CCC CGC	672
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg	
210 215 220	
GAG GAG CAG TAC AAC AGC ACC TTC CGC GTG GTG AGC GTG CTG ACC GTG	720
Glu Glu Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val	
225 230 235	
CTG CAC CAG GAC TGG CTG AAC GGC AAG GAG TAC AAG TGC AAG GTG AGC	768
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser	
240 245 250	
AAC AAG GCC CTG CCC GCC CCC ATC GAG AAG ACC ATC TCC AAG ACC AAG	816
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys	
255 260 265 270	
GGC CAG CCC CGC GAG CCC CAG GTG TAC ACC CTG CCC CCC AGC CGC GAG	864
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu	
275 280 285	
GAG ATG ACC AAG AAC CAG GTG AGC CTG ACC TGC CTG GTG AAG GGC TTC	912
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe	
290 295 300	
TAC CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AGC GGC CAG CCC GAG	960
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu	
305 310 315	
AAC AAC TAC AAC ACC ACC CCC CCC ATG CTG GAC AGC GAC GGC AGC TTC	1008
Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe	
320 325 330	
TTC CTG TAC AGC AAG CTG ACC GTG GAC AAG AGC CGC TGG CAG CAG GGC	1056
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly	
335 340 345 350	

AAC ATC TTC TCC TGC AGC GTG ATG CAT GAG GCC CTG CAC AAC CGC TTC	1104
Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe	
355 360 365	

ACC CAG AAG AGC CTG AGC CTG AGC CCC GGC AAG TGATAGATCT	1147
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
370 375	

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg
1				5					10					15	
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
			20					25					30		
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
		35					40					45			
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
	50					55					60				
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
	65				70					75					80
Tyr	Thr	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
			85					90						95	
Arg	Val	Glu	Leu	Lys	Thr	Pro	Leu	Gly	Asp	Thr	Thr	His	Thr	Cys	Pro
			100					105					110		
Arg	Cys	Pro	Glu	Pro	Lys	Ser	Cys	Asp	Thr	Pro	Pro	Pro	Cys	Pro	Arg
		115					120					125			
Cys	Pro	Glu	Pro	Lys	Ser	Cys	Asp	Thr	Pro	Pro	Pro	Cys	Pro	Arg	Cys
	130					135					140				
Pro	Glu	Pro	Lys	Ser	Cys	Asp	Thr	Pro	Pro	Pro	Cys	Pro	Arg	Cys	Pro
	145				150					155				160	
Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
				165					170					175	
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
			180					185					190		
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Lys	Trp	Tyr
		195					200					205			
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu
	210					215					220				

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
 225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 245 250 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
 260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
 305 310 315 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
 325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
 340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
 355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 9..989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCGGCCGC	GCG	TCG	ACC	AAG	GGC	CCC	AGC	GTG	TTC	CCC	CTG	GCC	CCC	TGC	50
	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	
	1				5					10					
AGC	CGC	AGC	ACC	AGC	GAG	AGC	ACC	GCC	GCC	CTG	GGC	TGC	CTG	GTG	AAG
Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys
15					20					25				30	98
GAC	TAC	TTC	CCC	GAG	CCC	GTG	ACC	GTG	AGC	TGG	AAC	AGC	GGC	GCC	CTG
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu
				35				40					45		146
ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCC	GCC	GTG	CTG	CAG	AGC	AGC	GGC	CTG
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu
			50					55					60		194

TAC TCC CTG AGC AGC GTG GTG ACC GTG CCC AGC AGC AGC CTG GGC ACC	242
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
65 70 75	
AAG ACC TAC ACC TGC AAC GTG GAC CAC AAG CCC AGC AAC ACC AAG GTG	290
Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val	
80 85 90	
GAC AAG CGC GTG GAG AGC AAG TAC GGC CCC CCC TGC CCC AGC TGC CCC	338
Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro	
95 100 105 110	
GCC CCC GAG TTC CTG GGC GGC CCC AGC GTG TTC CTG TTC CCC CCC AAG	386
Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys	
115 120 125	
CCC AAG GAC ACC CTG ATG ATC AGC CGC ACC CCC GAG GTG ACC TGC GTG	434
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val	
130 135 140	
GTG GTG GAC GTG AGC CAG GAG GAC CCC GAG GTG CAG TTC AAC TGG TAC	482
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr	
145 150 155	
GTG GAC GGC GTG GAG GTG CAT AAC GCC AAG ACC AAG CCC CGC GAG GAG	530
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu	
160 165 170	
CAG TTC AAC AGC ACC TAC CGC GTG GTG AGC GTG CTG ACC GTG CTG CAC	578
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His	
175 180 185 190	
CAG GAC TGG CTG AAC GGC AAG GAG TAC AAG TGC AAG GTG TCC AAC AAG	626
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys	
195 200 205	
GGC CTG CCC AGC AGC ATC GAG AAG ACC ATC AGC AAG GCC AAG GGC CAG	674
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln	
210 215 220	
CCC CGC GAG CCC CAG GTG TAC ACC CTG CCC CCC AGC CAG GAG GAG ATG	722
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met	
225 230 235	
ACC AAG AAC CAG GTG AGC CTG ACC TGC CTG GTG AAG GGC TTC TAC CCC	770
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro	
240 245 250	
AGC GAC ATC GCC GTG GAG TGG GAG AGC AAC GGC CAG CCC GAG AAC AAC	818
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn	
255 260 265 270	
TAC AAG ACC ACC CCC CCC GTG CTG GAC AGC GAC GGC AGC TTC TTC CTG	866
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu	
275 280 285	
TAC AGC CGC CTG ACC GTG GAC AAG AGC CGC TGG CAG GAG GGC AAC GTG	914
Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val	
290 295 300	

TTC TCC TGC TCC GTG ATG CAT GAG GCC CTG CAC AAC CAC TAC ACC CAG 962
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
305 310 315

AAG AGC CTG AGC CTG AGC CTG GGC AAG TGATAGATCT 999
Lys Ser Leu Ser Leu Ser Leu Gly Lys
320 325

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	1	5	10	15
Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	20	25	30	
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	35	40	45	
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	50	55	60	
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	65	70	75	80
Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	85	90	95	
Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Ser	Cys	Pro	Ala	Pro	100	105	110	
Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	115	120	125	
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	130	135	140	
Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	145	150	155	160
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	165	170	175	
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	180	185	190	
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	195	200	205	
Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	210	215	220	

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285
 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320
 Leu Ser Leu Ser Leu Gly Lys
 325

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 9..326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCGGCCGC	ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT	50
	Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp	
1	5 10	
GAG CAG CTT AAG TCC GGA ACC GCC AGC GTG GTG TGC CTG CTG AAC AAC	98	
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn		
15	20 25 30	
TTC TAC CCC CGC GAG GCC AAG GTG CAG TGG AAG GTG GAC AAC GCC CTC	146	
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu		
35	40 45	
CAG AGC GGC AAC TCC CAG GAG AGC GTG ACC GAG CAG GAC AGC AAG GAC	194	
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp		
50	55 60	
AGC ACC TAC AGC CTG AGC AGC ACC CTG ACC CTG AGC AAG GCC GAC TAC	242	
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr		
65	70 75	
GAG AAG CAC AAG GTG TAC GCC TGC GAG GTG ACC CAT CAG GGC CTG AGC	290	
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser		
80	85 90	

AGC CCC GTG ACC AAG AGC TTC AAC CGG GGC GAG TGC TAGTGAGATC 336
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 95 100 105

T 337

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1 5 10 15
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 20 25 30
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 35 40 45
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 50 55 60
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 65 70 75 80
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 85 90 95
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 100 105

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 9..335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCGGCCGC ACC GTC CTA GGT CAG CCC AAG GCG GCG CCC AGC GTG ACC CTG 50
 Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu
 1 5 10
 TTC CCC CCC AGC AGC GAG GAG CTG CAG GCC AAC AAG GCC ACC CTG GTG 98
 Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val
 15 20 25 30

TGC CTG ATC AGC GAC TTC TAC CCC GGG GCC GTG ACC GTG GCC TGG AAG	146
Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys	
35 40 45	
GCC GAC AGC AGC CCC GTG AAG GCC GGC GTG GAG ACC ACC ACC CCC AGC	194
Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser	
50 55 60	
AAG CAG AGC AAC AAC AAG TAC GCC GCC AGC AGC TAC CTG AGC CTG ACC	242
Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr	
65 70 75	
CCC GAG CAG TGG AAG AGC CAC CGC AGC TAC AGC TGC CAG GTC ACC CAC	290
Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His	
80 85 90	
GAG GGC AGC ACC GTG GAG AAG ACC GTG GCC CCC ACC GAG TGC AGC	335
Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser	
95 100 105	
TAGTGAGATC T	346

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro	
1 5 10 15	
Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu	
20 25 30	
Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp	
35 40 45	
Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln	
50 55 60	
Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu	
65 70 75 80	
Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly	
85 90 95	
Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser	
100 105	

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TCTAGAATTC ACGCGTCCAC CATGGACTGG ACCTGGAG

38

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCTAGAATTC ACGCGTCCAC CATGGACACA CTTTGCTACA C

41

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TCTAGAATTC ACGCGTCCAC CATGGAGTTT GGGCTGAGCT GG

42

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TCTAGAATTC ACGCGTCCAC CATGAAACAC CTGTGGTTCT TCCT

44

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TCTAGAATTC ACGCGTCCAC CATGGGGTCA ACCGCCATCC T

41

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TCTAGAATTC ACGCGTCCAC CATGTCTGTC TCCTTCCTCA TCTT

44

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCCTGAGTTC CACGACACCG TCAC

24

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGGGAAAAGG GTTGGGGCGG ATGC

24

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GAGGGGCCCT TGGTCGACGC TGAGGAGACG GTGACCAGG 39

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAGGGGCCCT TGGTCGACGC TGAAGAGACG GTGACCATTG 40

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAGGGGCCCT TGGTCGACGC TGAGGAGACG GTGACCGTG 39

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TCTAGAATTC ACGCGTCCAC CATGGACATG AGGGTCCCCG CTCAG 45

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TCTAGAATTC ACGCGTCCAC CATGAGGCTC CCTGCTCAGC

40

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTAGAATTC ACGCGTCCAC CATGGAAGCC CCAGCGCAGC TT

42

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TCTAGAATTC ACGCGTCCAC CATGGTGTG CAGACCCAGG T

41

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TCTAGAATTC ACGCGTCCAC CATGGGGTCC CAGGTTACC T

41

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TCTAGAATTC ACGCGTCCAC CATGTTGCCA TCACAACTCA TTG

43

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TCTAGAATTC ACGCGTCCAC CATGGTGTCC CCGTTGCAAT T

41

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GGTTCCGGAC TTAAGCTGCT CATCAGATGG CGGG

34

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TCTAGAATTC ACGCGTCCAC CATGGCCTGC TCTCCTCTCC TCCT

44

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TCTAGAATTC ACGCGTCCAC CATGGCCTGG GCTCTGCTGC TCCT

44

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TCTAGAATTC ACGCGTCCAC CATGGCCTGG ATCCTTCTCC TCCTC

45

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TCTAGAATTC ACGCGTCCAC CATGGCCTGG ACCCCTCTCT GGCTC

45

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TCTAGAATTC ACGCGTCCAC CATGGCCTGG GCCCACTAC T

41

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TCTAGAATTC ACGCGTCCAC CATGGCCTGG ATGATGCTTC TCCT

44

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCGCCGCCT TGGGCTGACC TAGGACGGT

29